

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/529,381

Source: PCT

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PCT

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DATE: 09/21/2005

PATENT APPLICATION: US/10/529,381

TIME: 14:25:34

Input Set : N:\Crf4\Refhold\10_folder\J529381.raw
Output Set: N:\CRF4\09212005\J529381.raw

1 <110> APPLICANT: Nakamura, Yusuke
2 Katagiri, Toyomasa
3 Nakagawa, Hidewaki
4 Nakatsuru, Shuichi
5 Oncotherapy Science, Inc.
6 The University of Tokyo
7 <120> TITLE OF INVENTION: GENES AND POLYPEPTIDES RELATING TO
8 PROSTATE CANCERS
9 <130> FILE REFERENCE: 082368-002810US
10 <140> CURRENT APPLICATION NUMBER: US/10/529,381
11 <141> CURRENT FILING DATE: 2005-03-28
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/12074
13 <151> PRIOR FILING DATE: 2003-09-22
14 <150> PRIOR APPLICATION NUMBER: US 60/414,873
15 <151> PRIOR FILING DATE: 2002-09-30
16 <160> NUMBER OF SEQ ID NOS: 28
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 826
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (332)..(634)
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30 aaaaggatca cagatggaga gacattttgc cacacgatga atcacacacc acatctcatc 180
31 cccgagcttc agctgcagga caatgctgcc agaggcctgg tcctcagagc tcacgtaagc 240
32 atctctgggtg tgcagtattt ttactccgtt tttgaccaa gacacctgaa cattcctgga 300
33 gaaaacagtg atgtggatct tatcaaattt a atg ggc aca tct gaa gaa gga 352
34 Met Gly Thr Ser Glu Glu Gly
35 1 5
36 aac ttg ctc agc acc gtg agc ccc aca gtg aaa gca ctt ttt ggc aag 400
37 Asn Leu Leu Ser Thr Val Ser Pro Thr Val Lys Ala Leu Phe Gly Lys
38 10 15 20
39 act aga gtc tca ccg att ttc cct ttc tct cct cga tct cct ttc cag 448
40 Thr Arg Val Ser Pro Ile Phe Pro Phe Ser Pro Arg Ser Pro Phe Gln
41 25 30 35
42 cct ctt att ccc cgg act cct ggc tca ccc tgg ggc ccc gtg ggt cca 496
43 Pro Leu Ile Pro Arg Thr Pro Gly Ser Pro Trp Gly Pro Val Gly Pro
44 40 45 50 55

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47      60      65      70
48      aaa cca gtt ggg ccc aaa ggc cca atg ttg ccc ctt ggc ccc tca gga      592
49      Lys Pro Val Gly Pro Lys Gly Pro Met Leu Pro Leu Gly Pro Ser Gly
50      75      80      85
51      cca gtg gga ccc acg tca ccc tta ttc ccc ttc tgc ccc tga      634
52      Pro Val Gly Pro Thr Ser Pro Leu Phe Pro Phe Cys Pro
53      90      95      100
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55      tgttttcctg gggatcctct tgagccttga tcacctttga tgccttttgc ttcaactttt      754
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61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
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67      20      25      30
68      Ser Pro Arg Ser Pro Phe Gln Pro Leu Ile Pro Arg Thr Pro Gly Ser
69      35      40      45
70      Pro Trp Gly Pro Val Gly Pro Ala Ser Pro Leu Gly Pro Gly Phe Pro
71      50      55      60
72      Ile Gly Pro Met Gly Pro Gly Lys Pro Val Gly Pro Lys Gly Pro Met
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85 <222> LOCATION: (265)..(3195)
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90      atggcaaccc gtgtgtgtct catccagaa agagaagact ttaaccactg tgatgcctga      180
91      gaatccagtg tgacgtttct ccagataact catgtgttgc acctgtgtcc tcgcgcacc      240
92      actgcccac acgactcctg aacc atg ggg gaa aac gag gat gag aag cag      291
93      Met Gly Glu Asn Glu Asp Glu Lys Gln
94      1      5
95      gcc cag gcg ggg cag gtt ttt gag aac ttt gtc cag gca tcc acg tgc      339
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96	Ala Gln Ala Gly Gln Val Phe Glu Asn Phe Val Gln Ala Ser Thr Cys	
97	10 15 20 25	
98	aaa ggt acc ctc cag gcc ttc aac att ctc aca cga cac ctg gac cta	387
99	Lys Gly Thr Leu Gln Ala Phe Asn Ile Leu Thr Arg His Leu Asp Leu	
100	30 35 40	
101	gac cct ctg gac cac aga aac ttt tat tcc aag ctc aag tcc aag gtg	435
102	Asp Pro Leu Asp His Arg Asn Phe Tyr Ser Lys Leu Lys Ser Lys Val	
103	45 50 55	
104	acc acc tgg aaa gcc aaa gcc ctg tgg tac aaa ttg gat aag cgt ggt	483
105	Thr Thr Trp Lys Ala Lys Ala Leu Trp Tyr Lys Leu Asp Lys Arg Gly	
106	60 65 70	
107	tcc cac aaa gag tat aag cga ggg aag tct tgc acg aac acc aag tgt	531
108	Ser His Lys Glu Tyr Lys Arg Gly Lys Ser Cys Thr Asn Thr Lys Cys	
109	75 80 85	
110	ctc ata gtt ggg gga gga ccc tgt ggc ttg cgc act gcc att gaa ctt	579
111	Leu Ile Val Gly Gly Gly Pro Cys Gly Leu Arg Thr Ala Ile Glu Leu	
112	90 95 100 105	
113	gcc tac ctg gga gcc aaa gtg gtc gtg gtg gag aag agg gac tcc ttc	627
114	Ala Tyr Leu Gly Ala Lys Val Val Val Val Glu Lys Arg Asp Ser Phe	
115	110 115 120	
116	tcc cgg aac aac gtg cta cac ctc tgg cct ttc acc atc cat gac ctt	675
117	Ser Arg Asn Asn Val Leu His Leu Trp Pro Phe Thr Ile His Asp Leu	
118	125 130 135	
119	cgg ggc ctg gga gcc aag aag ttc tat ggg aag ttc tgt gct ggc tcc	723
120	Arg Gly Leu Gly Ala Lys Lys Phe Tyr Gly Lys Phe Cys Ala Gly Ser	
121	140 145 150	
122	atc gac cat atc agt att cgc caa cta cag ctc atc cta ttc aag gtg	771
123	Ile Asp His Ile Ser Ile Arg Gln Leu Gln Leu Ile Leu Phe Lys Val	
124	155 160 165	
125	gcc ctg atg ctg gga gtt gaa atc cat gtg aat gtg gag ttc gtg aag	819
126	Ala Leu Met Leu Gly Val Glu Ile His Val Asn Val Glu Phe Val Lys	
127	170 175 180 185	
128	gtt cta gag cct cct gaa gat caa gaa aat caa aaa att ggc tgg cgg	867
129	Val Leu Glu Pro Pro Glu Asp Gln Glu Asn Gln Lys Ile Gly Trp Arg	
130	190 195 200	
131	gca gaa ttt ctc cct aca gac cat tct ctg tct gag ttt gag ttt gac	915
132	Ala Glu Phe Leu Pro Thr Asp His Ser Leu Ser Glu Phe Glu Phe Asp	
133	205 210 215	
134	gtc atc att ggt gcc gat ggc cgc agg aac acc ctg gaa ggg ttc aga	963
135	Val Ile Ile Gly Ala Asp Gly Arg Arg Asn Thr Leu Glu Gly Phe Arg	
136	220 225 230	
137	aga aaa gaa ttc cgt ggg aag ctg gcg att gcc atc acc gcc aac ttc	1011
138	Arg Lys Glu Phe Arg Gly Lys Leu Ala Ile Ala Ile Thr Ala Asn Phe	
139	235 240 245	
140	ata aac aga aac agc aca gcg gaa gcc aag gtg gaa gag att agt ggt	1059
141	Ile Asn Arg Asn Ser Thr Ala Glu Ala Lys Val Glu Glu Ile Ser Gly	
142	250 255 260 265	
143	gtg gct ttc atc ttc aat cag aaa ttt ttt cag gac ctt aaa gaa gaa	1107
144	Val Ala Phe Ile Phe Asn Gln Lys Phe Phe Gln Asp Leu Lys Glu Glu	

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145		270		275		280		
146	aca ggc ata gat ctt gag aac att gtt tac tac aag gac tgc acc cac							1155
147	Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys Asp Cys Thr His							
148		285		290		295		
149	tat ttt gta atg aca gcc aag aag cag agc ctg ctc gac aaa ggt gtc							1203
150	Tyr Phe Val Met Thr Ala Lys Lys Gln Ser Leu Leu Asp Lys Gly Val							
151		300		305		310		
152	atc att aac gac tac atc gac aca gag atg ctg ctg tgt gcg gag aac							1251
153	Ile Ile Asn Asp Tyr Ile Asp Thr Glu Met Leu Leu Cys Ala Glu Asn							
154		315		320		325		
155	gtg aac caa gac aac ctg cta tcc tat gcc cgg gaa gct gca gac ttt							1299
156	Val Asn Gln Asp Asn Leu Ser Tyr Ala Arg Glu Ala Ala Asp Phe							
157		330		335		340		345
158	gcc acc aac tac cag ctg cca tcc tta gac ttt gcc atg aac cac tat							1347
159	Ala Thr Asn Tyr Gln Leu Pro Ser Leu Asp Phe Ala Met Asn His Tyr							
160		350		355		360		
161	ggg cag cct gat gtg gcc atg ttt gac ttt acc tgc atg tat gcc tca							1395
162	Gly Gln Pro Asp Val Ala Met Phe Asp Phe Thr Cys Met Tyr Ala Ser							
163		365		370		375		
164	gag aac gcg gcc ctg gtg cgg gag cgg cag gcg cac cag ctg ctc gtg							1443
165	Glu Asn Ala Ala Leu Val Arg Glu Arg Gln Ala His Gln Leu Leu Val							
166		380		385		390		
167	gcc ctt gtg ggt gac agc ttg ctt gag cca ttt tgg ccc atg ggt aca							1491
168	Ala Leu Val Gly Asp Ser Leu Leu Glu Pro Phe Trp Pro Met Gly Thr							
169		395		400		405		
170	ggc tgt gcc cgt ggc ttc ctg gca gcc ttt gac acg gca tgg atg gtg							1539
171	Gly Cys Ala Arg Gly Phe Leu Ala Ala Phe Asp Thr Ala Trp Met Val							
172		410		415		420		425
173	aag agc tgg aac cag ggc acc cct ccc ctg gag ctg ctg gct gaa agg							1587
174	Lys Ser Trp Asn Gln Gly Thr Pro Pro Leu Glu Leu Leu Ala Glu Arg							
175		430		435		440		
176	gaa agt ctc tac cgg ctg tta cct cag aca acc ccg gag aac atc aac							1635
177	Glu Ser Leu Tyr Arg Leu Leu Pro Gln Thr Thr Pro Glu Asn Ile Asn							
178		445		450		455		
179	aag aac ttt gag cag tac acg ttg gac cca ggg aca cgg tac cca aac							1683
180	Lys Asn Phe Glu Gln Tyr Thr Leu Asp Pro Gly Thr Arg Tyr Pro Asn							
181		460		465		470		
182	ctc aac tca cac tgt gtc agg ccc cat cag gtg aag cat ttg tat atc							1731
183	Leu Asn Ser His Cys Val Arg Pro His Gln Val Lys His Leu Tyr Ile							
184		475		480		485		
185	act aag gag ctg gag cac tac cct ctc gag aga ctg ggc tcg gtg agg							1779
186	Thr Lys Glu Leu Glu His Tyr Pro Leu Glu Arg Leu Gly Ser Val Arg							
187		490		495		500		505
188	aga tct gtc aac ctc tcc agg aag gag tca gat atc cgg ccc agc aag							1827
189	Arg Ser Val Asn Leu Ser Arg Lys Glu Ser Asp Ile Arg Pro Ser Lys							
190		510		515		520		
191	ctc ctg acc tgg tgc cag cag cag aca gag ggc tac cag cat gtc aac							1875
192	Leu Leu Thr Trp Cys Gln Gln Gln Thr Glu Gly Tyr Gln His Val Asn							
193		525		530		535		

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196	540 545 550	
197	atc atc cac cgc ttc cgg cct gag ctc atc aac ttt gac tct ttg aat	1971
198	Ile Ile His Arg Phe Arg Pro Glu Leu Ile Asn Phe Asp Ser Leu Asn	
199	555 560 565	
200	gaa gat gat gct gtg gag aac aac cag ctc gca ttt gat gtg gcc gag	2019
201	Glu Asp Asp Ala Val Glu Asn Asn Gln Leu Ala Phe Asp Val Ala Glu	
202	570 575 580 585	
203	cga gag ttt ggg atc cct cca gtg acc acg ggc aaa gag atg gca tct	2067
204	Arg Glu Phe Gly Ile Pro Pro Val Thr Thr Gly Lys Glu Met Ala Ser	
205	590 595 600	
206	gcc cag gag cct gac aag ctc agc atg gtc atg tac ctc tcc aag ttc	2115
207	Ala Gln Glu Pro Asp Lys Leu Ser Met Val Met Tyr Leu Ser Lys Phe	
208	605 610 615	
209	tac gag ctc ttc cgg ggc acc cca ctg agg ccc gtg gat tct tgg cgc	2163
210	Tyr Glu Leu Phe Arg Gly Thr Pro Leu Arg Pro Val Asp Ser Trp Arg	
211	620 625 630	
212	aaa aac tat gga gaa aat gct gac ctc agc ttg gcc aaa tca tcc att	2211
213	Lys Asn Tyr Gly Glu Asn Ala Asp Leu Ser Leu Ala Lys Ser Ser Ile	
214	635 640 645	
215	tct aat aac tat ctc aac ctc aca ttt cca agg aag agg act cca cgg	2259
216	Ser Asn Asn Tyr Leu Asn Leu Thr Phe Pro Arg Lys Arg Thr Pro Arg	
217	650 655 660 665	
218	gtg gat ggt caa acc gga gag aat gac atg aac aaa cgg aga cgg aag	2307
219	Val Asp Gly Gln Thr Gly Glu Asn Asp Met Asn Lys Arg Arg Arg Lys	
220	670 675 680	
221	ggc ttc acc aac ctg gac gag cct tca aac ttt tcc agc cgt agc ttg	2355
222	Gly Phe Thr Asn Leu Asp Glu Pro Ser Asn Phe Ser Ser Arg Ser Leu	
223	685 690 695	
224	ggc tcc aat caa gag tgt ggg agc agt aag gaa ggt gga aat cag aac	2403
225	Gly Ser Asn Gln Glu Cys Gly Ser Ser Lys Glu Gly Gly Asn Gln Asn	
226	700 705 710	
227	aaa gtc aag tcc atg gcg aat cag ctg ctg gcc aag ttt gag gag agc	2451
228	Lys Val Lys Ser Met Ala Asn Gln Leu Leu Ala Lys Phe Glu Glu Ser	
229	715 720 725	
230	act cgg aac ccc tca ctc atg aag cag gaa aag aag tca cct tca ggg	2499
231	Thr Arg Asn Pro Ser Leu Met Lys Gln Glu Lys Lys Ser Pro Ser Gly	
232	730 735 740 745	
233	ttc cat ttt cat ccc agc cat ttg aga aca gtg cat cct cag gaa tct	2547
234	Phe His Phe His Pro Ser His Leu Arg Thr Val His Pro Gln Glu Ser	
235	750 755 760	
236	atg cga aag tca ttt ccc ctt aac ctg gga ggc agc gac acg tgt tac	2595
237	Met Arg Lys Ser Phe Pro Leu Asn Leu Gly Gly Ser Asp Thr Cys Tyr	
238	765 770 775	
239	ttc tgt aag aaa cgt gtg tac gtg atg gaa cgg ctg agc gcc gag ggc	2643
240	Phe Cys Lys Lys Arg Val Tyr Val Met Glu Arg Leu Ser Ala Glu Gly	
241	780 785 790	
242	cac ttc ttc cac cgg gag tgt ttc cgc tgc agc atc tgt gcc acc acc	2691

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Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28

VERIFICATION SUMMARY

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Output Set: N:\CRF4\09212005\J529381.raw

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L:87 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
L:475 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0